

SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rnnpn.

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This page gives you Search Results detail for the Application 10063581 and Search Result us-10-063-581-72.rnnpn.

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 6, 2006, 17:16:35 ; Search time 146 Seconds
(without alignments)
2307.745 Million cell updates/sec

Title: US-10-063-581-72
Perfect score: 2802
Sequence: 1 MMMVRRGLLAWISRVVLLV.....RHEIEAHLRKQKQKTSSKKT 532

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 251160 seqs, 211109531 residues

Total number of hits satisfying chosen parameters: 502320

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10063581/runat_06062006_121416_12300/app_query.fasta_1
-DB=Pending_Patents_NA_New -QFMT=fastap -SUFFIX=rnnpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_New:*
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3: /EMC_Celerra_SIDS3/ptodata/2/pna/US07_NEW_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|---------------------|-------------------|
| 1 | 2740 | 97.8 | 3359 | 7 | US-11-433-832-5826 | Sequence 5826, Ap |
| 2 | 370 | 13.2 | 282 | 7 | US-11-433-832-46533 | Sequence 46533, A |
| 3 | 361.5 | 12.9 | 519 | 7 | US-11-433-832-35532 | Sequence 35532, A |
| 4 | 220 | 7.9 | 182 | 7 | US-11-433-832-25047 | Sequence 25047, A |
| 5 | 127 | 4.5 | 711 | 7 | US-11-433-832-11536 | Sequence 11536, A |
| 6 | 109 | 3.9 | 3015 | 1 | PCT-US03-41389-555 | Sequence 555, App |
| 7 | 109 | 3.9 | 3027 | 1 | PCT-US03-41389-557 | Sequence 557, App |
| 8 | 107.5 | 3.8 | 6025 | 7 | US-11-431-708-4455 | Sequence 4455, Ap |
| 9 | 107.5 | 3.8 | 6025 | 7 | US-11-437-729-4648 | Sequence 4648, Ap |
| 10 | 107.5 | 3.8 | 6148 | 7 | US-11-431-708-4449 | Sequence 4449, Ap |
| 11 | 107.5 | 3.8 | 6148 | 7 | US-11-431-708-4452 | Sequence 4452, Ap |
| 12 | 107.5 | 3.8 | 6148 | 7 | US-11-437-729-4636 | Sequence 4636, Ap |
| 13 | 107.5 | 3.8 | 6148 | 7 | US-11-437-729-4650 | Sequence 4650, Ap |
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| 16 | 107.5 | 3.8 | 6187 | 7 | US-11-431-708-4443 | Sequence 4443, Ap |
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| 26 | 105.5 | 3.8 | 2300 | 7 | US-11-414-676-3 | Sequence 3, Appli |
| 27 | 105.5 | 3.8 | 2312 | 7 | US-11-433-832-48093 | Sequence 48093, A |
| 28 | 105.5 | 3.8 | 3138 | 8 | US-60-796-903-19 | Sequence 19, Appl |
| 29 | 105.5 | 3.8 | 4512 | 7 | US-11-433-832-27189 | Sequence 27189, A |
| 30 | 105 | 3.7 | 5998 | 7 | US-11-437-729-3901 | Sequence 3901, Ap |
| 31 | 105 | 3.7 | 7448 | 7 | US-11-437-729-3902 | Sequence 3902, Ap |
| 32 | 105 | 3.7 | 7448 | 7 | US-11-437-729-3903 | Sequence 3903, Ap |
| 33 | 105 | 3.7 | 8969 | 1 | PCT-US03-41389-38 | Sequence 38, Appl |
| 34 | 104 | 3.7 | 2788 | 7 | US-11-433-832-603 | Sequence 603, App |
| 35 | 103.5 | 3.7 | 14198 | 7 | US-11-437-729-5075 | Sequence 5075, Ap |
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| 37 | 101.5 | 3.6 | 1717 | 7 | US-11-253-199-2166 | Sequence 2166, Ap |
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| | | | | |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
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http://es/ScoreAccessWeb/GetItem.action?AppId=10063581&seqId=532467&ItemName=us-... 6/8/06

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|--------------------|-------------------|
| 1 | 2802 | 100.0 | 1746 | 8 | US-10-698-190-13 | Sequence 13, Appl |
| 2 | 2802 | 100.0 | 3877 | 3 | US-09-989-722-380 | Sequence 380, App |
| 3 | 2802 | 100.0 | 3877 | 3 | US-09-989-723-380 | Sequence 380, App |
| 4 | 2802 | 100.0 | 3877 | 3 | US-09-989-279-380 | Sequence 380, App |
| 5 | 2802 | 100.0 | 3877 | 3 | US-09-989-727-380 | Sequence 380, App |
| 6 | 2802 | 100.0 | 3877 | 3 | US-09-989-731-380 | Sequence 380, App |
| 7 | 2802 | 100.0 | 3877 | 3 | US-09-989-732-380 | Sequence 380, App |
| 8 | 2802 | 100.0 | 3877 | 3 | US-09-991-073-380 | Sequence 380, App |
| 9 | 2802 | 100.0 | 3877 | 3 | US-09-990-442-380 | Sequence 380, App |
| 10 | 2802 | 100.0 | 3877 | 3 | US-09-991-163-380 | Sequence 380, App |
| 11 | 2802 | 100.0 | 3877 | 3 | US-09-993-604-380 | Sequence 380, App |
| 12 | 2802 | 100.0 | 3877 | 3 | US-09-990-456-380 | Sequence 380, App |
| 13 | 2802 | 100.0 | 3877 | 3 | US-09-989-721-380 | Sequence 380, App |
| 14 | 2802 | 100.0 | 3877 | 3 | US-09-992-598-380 | Sequence 380, App |
| 15 | 2802 | 100.0 | 3877 | 3 | US-09-989-293A-380 | Sequence 380, App |
| 16 | 2802 | 100.0 | 3877 | 3 | US-09-989-735-380 | Sequence 380, App |
| 17 | 2802 | 100.0 | 3877 | 3 | US-09-990-444-380 | Sequence 380, App |
| 18 | 2802 | 100.0 | 3877 | 3 | US-09-991-181-380 | Sequence 380, App |
| 19 | 2802 | 100.0 | 3877 | 3 | US-09-989-730-380 | Sequence 380, App |
| 20 | 2802 | 100.0 | 3877 | 3 | US-09-990-436-380 | Sequence 380, App |
| 21 | 2802 | 100.0 | 3877 | 3 | US-09-993-687-380 | Sequence 380, App |
| 22 | 2802 | 100.0 | 3877 | 3 | US-09-989-734-380 | Sequence 380, App |
| 23 | 2802 | 100.0 | 3877 | 3 | US-09-997-653-380 | Sequence 380, App |
| 24 | 2802 | 100.0 | 3877 | 3 | US-09-989-724-380 | Sequence 380, App |
| 25 | 2802 | 100.0 | 3877 | 3 | US-09-989-728-380 | Sequence 380, App |
| 26 | 2802 | 100.0 | 3877 | 3 | US-09-990-441-380 | Sequence 380, App |
| 27 | 2802 | 100.0 | 3877 | 3 | US-09-993-667-380 | Sequence 380, App |
| 28 | 2802 | 100.0 | 3877 | 3 | US-09-997-428-380 | Sequence 380, App |
| 29 | 2802 | 100.0 | 3877 | 3 | US-09-997-666-380 | Sequence 380, App |
| 30 | 2802 | 100.0 | 3877 | 3 | US-09-990-438-380 | Sequence 380, App |
| 31 | 2802 | 100.0 | 3877 | 3 | US-09-990-562-380 | Sequence 380, App |
| 32 | 2802 | 100.0 | 3877 | 3 | US-09-990-711-380 | Sequence 380, App |
| 33 | 2802 | 100.0 | 3877 | 3 | US-09-989-726-380 | Sequence 380, App |
| 34 | 2802 | 100.0 | 3877 | 3 | US-09-998-156-380 | Sequence 380, App |
| 35 | 2802 | 100.0 | 3877 | 3 | US-09-990-437-380 | Sequence 380, App |

SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rnpbn.

| | | | | |
|---------------------------------|---|---------------------------------------|---------------------------|--|
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|---------------------------------|---|---------------------------------------|---------------------------|--|

This page gives you Search Results detail for the Application 10063581 and Search Result us-10-063-581-72.rnpbn.

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 6, 2006, 19:36:54 ; Search time 31 Seconds
(without alignments)
3031.730 Million cell updates/sec

Title: US-10-063-581-72
Perfect score: 2802
Sequence: 1 MMMVRRGLLAWISRVVLLV.....RHEIEAHLRKQKQKTSSKKT 532

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10063581/runat_06062006_121423_12406/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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Database : Published_Applications_NA_New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % | | DB | ID | Description |
|------------|-------|-------------|--------|----|----------------------|-------------------|
| | | Query Match | Length | | | |
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| 2 | 2802 | 100.0 | 3877 | 7 | US-11-101-316-71 | Sequence 71, Appl |
| 3 | 2798 | 99.9 | 3426 | 6 | US-10-511-937-438 | Sequence 438, App |
| 4 | 529.5 | 18.9 | 4563 | 6 | US-10-196-749-311 | Sequence 311, App |
| 5 | 253.5 | 9.0 | 1823 | 7 | US-11-293-697-2080 | Sequence 2080, Ap |
| 6 | 108.5 | 3.9 | 1625 | 6 | US-10-953-349-17058 | Sequence 17058, A |
| 7 | 106.5 | 3.8 | 1956 | 7 | US-11-217-529-76687 | Sequence 76687, A |
| 8 | 106 | 3.8 | 5040 | 7 | US-11-217-529-77055 | Sequence 77055, A |
| 9 | 106 | 3.8 | 10211 | 6 | US-10-505-928-326 | Sequence 326, App |
| 10 | 105 | 3.7 | 1680 | 7 | US-11-217-529-3752 | Sequence 3752, Ap |
| 11 | 105 | 3.7 | 2139 | 7 | US-11-217-529-1868 | Sequence 1868, Ap |
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| 18 | 98.5 | 3.5 | 1944 | 7 | US-11-217-529-78837 | Sequence 78837, A |
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| 23 | 94.5 | 3.4 | 1964 | 7 | US-11-101-316-41 | Sequence 41, Appl |
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SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rni.

| | | | | |
|---------------------------------|---|---------------------------------------|---------------------------|--|
| Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions |
|---------------------------------|---|---------------------------------------|---------------------------|--|

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 6, 2006, 17:07:30 ; Search time 293 Seconds
(without alignments)
5096.057 Million cell updates/sec

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Perfect score: 2802
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 35 | 215.5 | 7.7 | 2988 | 3 | US-09-992-598-325 | Sequence 325, App | |
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SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rapn.

| | | | | |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
| Score Home | Retrieve Application | SCORE System | SCORE | Comments / |
| Page | List | Overview | FAQ | Suggestions |

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OM protein - protein search, using sw model

Run on: June 6, 2006, 18:27:46 ; Search time 25 Seconds
(without alignments)
681.506 Million cell updates/sec

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Perfect score: 2802
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 131829

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

US-11-437-729-2073

; Sequence 2073, Application US/11437729

; GENERAL INFORMATION:

; APPLICANT: JOSELOFF, Elizabeth et al.

; TITLE OF INVENTION: STOMACH DISEASE TARGETS AND USES THEREOF

; FILE REFERENCE: CL001606

; CURRENT APPLICATION NUMBER: US/11/437,729

; CURRENT FILING DATE: 2006-05-22

SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rapm.

| | | | | |
|---------------------------------|---|---------------------------------------|---------------------------|--|
| Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions |
|---------------------------------|---|---------------------------------------|---------------------------|--|

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OM protein - protein search, using sw model

Run on: June 6, 2006, 18:26:45 ; Search time 610 Seconds
(without alignments)
1331.706 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 12 | 2802 | 100.0 | 532 | 29 | US-09-989-729A-381 | Sequence 381, App |
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SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rapbn.

| | | | | |
|---------------------------------|---|---------------------------------------|---------------------------|--|
| Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions |
|---------------------------------|---|---------------------------------------|---------------------------|--|

This page gives you Search Results detail for the Application 10063581 and Search Result us-10-063-581-72.rapbn.

[start](#)

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2006, 18:38:31 ; Search time 16 Seconds
(without alignments)
384.541 Million cell updates/sec

Title: US-10-063-581-72
Perfect score: 2802
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | |
|--------|------------|
| Result | % Query |
|--------|------------|

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| 3 | 2798 | 99.9 | 532 | 6 | US-10-511-937-2495 | Sequence 2495, Ap |
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| 7 | 108.5 | 3.9 | 515 | 6 | US-10-953-349-17060 | Sequence 17060, A |
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| 13 | 95.5 | 3.4 | 525 | 6 | US-10-953-349-32293 | Sequence 32293, A |
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| 15 | 95.5 | 3.4 | 670 | 6 | US-10-953-349-32291 | Sequence 32291, A |
| 16 | 94.5 | 3.4 | 344 | 6 | US-10-196-749-178 | Sequence 178, App |
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| 18 | 93 | 3.3 | 244 | 6 | US-10-953-349-30986 | Sequence 30986, A |
| 19 | 92.5 | 3.3 | 682 | 7 | US-11-293-697-4510 | Sequence 4510, Ap |
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| 21 | 92 | 3.3 | 590 | 6 | US-10-953-349-14233 | Sequence 14233, A |
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| 25 | 90 | 3.2 | 363 | 7 | US-11-293-697-4314 | Sequence 4314, Ap |
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| 27 | 90 | 3.2 | 460 | 6 | US-10-953-349-2818 | Sequence 2818, Ap |
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| 30 | 90 | 3.2 | 950 | 7 | US-11-293-697-4492 | Sequence 4492, Ap |
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ALIGNMENTS

RESULT 1

US-10-196-749-264
 ; Sequence 264, Application US/10196749
 ; Publication No. US20060094864A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey

SCORE Search Results Details for Application 10063581 and Search Result us-10-063-581-72.rapbm.

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2006, 18:38:06 ; Search time 187 Seconds
(without alignments)
1317.809 Million cell updates/sec

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Scoring table: BLOSUM62
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

```

| | | | | |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
| Score Home | Retrieve Application | SCORE System | SCORE | Comments / |
| Page | List | Overview | FAQ | Suggestions |

start

[Go Back to previous page](#)

OM protein - protein search, using sw model

Title: US-10-063-581-72
Perfect score: 2802
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Total number of hits satisfying chosen parameters: 650591

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 7 | 2802 | 100.0 | 532 | 3 | US-09-997-514-381 | Sequence 381, App |
| 8 | 2802 | 100.0 | 532 | 3 | US-09-989-728-381 | Sequence 381, App |
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| 40 | 215.5 | 7.7 | 775 | 3 | US-09-997-349-326 | Sequence 326, App |
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; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

```